



SEQUENCE LISTING

<110> DELEERSNIJDER, WILLY
WEESP, GUY NYS
VENEMA, JAKOB
BERGER, CLAUDIA
LOKEN, CHRISTIANE

<120> HUMAN G-PROTEIN COUPLED RECEPTOR

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<140> 10/088,744

<141> 2002-03-22

<160> 35

<170> PatentIn Ver. 3.2

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Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys
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cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg 153
Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu
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Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
35 40 45

gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg 249
Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu
50 55 60 65

gtg tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac 297
Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn
70 75 80

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Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu	
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gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg	393
Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu	
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Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr	
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Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe	
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Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro	
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Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro	
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Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr	
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Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn	
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Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu	
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Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu	
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Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala
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Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys
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cac ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cca tgt cag 1209
His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys Gln
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Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln
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Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
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Ser	Val	Val	Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	50	55	60
Leu	Val	Cys	Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr	65	70	75
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Tyr	Leu	Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	225	230	235
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Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys
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gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156
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Tyr	Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	Leu	Gly	
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gcc	ctc	agg	atc	ctc	ggc	atc	gtc	tgg	ggc	ttc	tcc	gtg	ctc	ttc	tcc	588
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Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	
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Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	Leu	
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Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr	
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Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	Leu	Val	Cys	50	55	60	
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Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe	Leu	Phe	Gly	100	105	110	
Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr	Val	Cys	Phe	115	120	125	
Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr	Val	Ala	130	135	140	
Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg	Ala	145	150	155	160
Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	Ser	Leu	165	170	175	
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Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	Arg	Leu	225	230	235	240
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 Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu
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 Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
 35 40 45

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Val	Cys	Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr	Asn	
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Phe	Gly	Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr	Val	
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		180					185					190				
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Asn	Gly	Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	
	195					200					205					
atg	tgg	atc	tac	aat	ttc	atc	atc	cag	gtc	acc	tcc	ttc	cta	ttc	tac	729
Met	Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	
210					215					220					225	
ctc	ctc	ccc	atg	act	gtc	atc	agt	gtc	ctc	tac	tac	ctc	atg	gca	ctc	777
Leu	Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	
				230					235					240		
aga	cta	aag	aaa	gac	aaa	tct	ctt	gag	gca	gat	gaa	ggg	aat	gca	aat	825
Arg	Leu	Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	
			245					250					255			

att caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg	873
Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu	
260 265 270	
gtc tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc	921
Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu	
275 280 285	
ttc ttc agc ttt gtg gag gag tgg act gaa tcc ctg gct gct gtg ttc	969
Phe Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val Phe	
290 295 300 305	
aac ctc gtc cat gtg gtg tca ggt gtc tta ttc tac ctg agc tca gct	1017
Asn Leu Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala	
310 315 320	
gtc aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca	1065
Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala	
325 330 335	
ttc cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat	1113
Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His	
340 345 350	
gac cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc	1161
Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys	
355 360 365	
cac ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cta tgt cag	1209
His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys Gln	
370 375 380 385	
tca tcc gtg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag	1257
Ser Ser Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln	
390 395 400	
atg tca aga aca aac tat caa agc ttc cac ttt aac aaa acc	1299
Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr	
405 410 415	
tgaattcttt cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat	1359
aatgtatgcc ttctcatatg aaattagaga ggtagaatgg ctcttacaac tcatgtaccc	1419
attgctagtt tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac	1479
ccaagactgc ctgattttta gttatctttc cactatccta actgcctcat gcccttcac	1539
tagttcatgc caagaacgtg actggaaagg catggcacct ataccttgat taatttccat	1599
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<210> 6
 <211> 415
 <212> PRT
 <213> Homo sapiens

<400> 6

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Lys	Leu	Glu	Asp	Pro	Phe	Gln	Lys	His	Leu	Asn	Ser	Thr	Glu	Glu	Tyr
			20					25					30		
Leu	Ala	Phe	Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val
		35					40					45			
Ser	Val	Val	Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val
	50					55					60				
Leu	Val	Cys	Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr
65					70					75					80
Asn	Tyr	Tyr	Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu
				85					90					95	
Leu	Gly	Met	Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe
			100					105					110		
Leu	Phe	Gly	Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr
		115					120					125			
Val	Cys	Phe	Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg
	130					135					140				
Tyr	Val	Ala	Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg
145					150					155					160
Arg	Arg	Ala	Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu
				165					170					175	
Phe	Ser	Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe
			180					185					190		
Pro	Asn	Gly	Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys
		195					200					205			
Pro	Met	Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe
	210					215					220				
Tyr	Leu	Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala
225					230					235					240
Leu	Arg	Leu	Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala
				245					250					255	

Asn	Ile	Gln	Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Phe	Val	
			260					265					270			
Leu	Val	Leu	Val	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Phe	His	Ile	Asp	Arg	
		275					280					285				
Leu	Phe	Phe	Ser	Phe	Val	Glu	Glu	Trp	Thr	Glu	Ser	Leu	Ala	Ala	Val	
	290					295					300					
Phe	Asn	Leu	Val	His	Val	Val	Ser	Gly	Val	Leu	Phe	Tyr	Leu	Ser	Ser	
305					310					315					320	
Ala	Val	Asn	Pro	Ile	Ile	Tyr	Asn	Leu	Leu	Ser	Arg	Arg	Phe	Gln	Ala	
				325					330					335		
Ala	Phe	Gln	Asn	Val	Ile	Ser	Ser	Phe	His	Lys	Gln	Trp	His	Ser	Gln	
			340					345					350			
His	Asp	Pro	Gln	Leu	Pro	Pro	Ala	Gln	Arg	Asn	Ile	Phe	Leu	Thr	Glu	
		355					360					365				
Cys	His	Phe	Val	Glu	Leu	Thr	Glu	Asp	Ile	Gly	Pro	Gln	Phe	Leu	Cys	
	370					375					380					
Gln	Ser	Ser	Val	His	Asn	Ser	His	Leu	Pro	Thr	Ala	Leu	Ser	Ser	Glu	
385					390					395					400	
Gln	Met	Ser	Arg	Thr	Asn	Tyr	Gln	Ser	Phe	His	Phe	Asn	Lys	Thr		
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<210> 7
<211> 1658
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (64)..(1299)
<223> IGS4B short version
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ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa cta 108
Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu
1 5 10 15

gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156
Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala
20 25 30

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ttc	ctc	tgc	gga	cct	cgg	cgc	agc	cac	ttc	ttc	ctc	ccc	gtg	tct	gtg	204
Phe	Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val	Ser	Val	
			35					40					45			
gtg	tat	gtg	cca	att	ttt	gtg	gtg	ggg	gtc	att	ggc	aat	gtc	ctg	gtg	252
Val	Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	Leu	Val	
		50					55					60				
tgc	ctg	gtg	att	ctg	cag	cac	cag	gct	atg	aag	acg	ccc	acc	aac	tac	300
Cys	Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr	Asn	Tyr	
	65					70					75					
tac	ctc	ttc	agc	ctg	gcg	gtc	tct	gac	ctc	ctg	gtc	ctg	ctc	ctt	gga	348
Tyr	Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	Leu	Gly	
	80				85					90					95	
atg	ccc	ctg	gag	gtc	tat	gag	atg	tgg	cgc	aac	tac	cct	ttc	ttg	ttc	396
Met	Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe	Leu	Phe	
			100						105					110		
ggg	ccc	gtg	ggc	tgc	tac	ttc	aag	acg	gcc	ctc	ttt	gag	acc	gtg	tgc	444
Gly	Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr	Val	Cys	
			115					120				125				
ttc	gcc	tcc	atc	ctc	agc	atc	acc	acc	gtc	agc	gtg	gag	cgc	tac	gtg	492
Phe	Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr	Val	
		130					135					140				
gcc	atc	cta	cac	ccg	ttc	cgc	gcc	aaa	ctg	cag	agc	acc	cgg	cgc	cgg	540
Ala	Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg	
	145					150					155					
gcc	ctc	agg	atc	ctc	ggc	atc	gtc	tgg	ggc	ttc	tcc	gtg	ctc	ttc	tcc	588
Ala	Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	Ser	
160					165					170					175	
ctg	ccc	aac	acc	agc	atc	cat	ggc	atc	aag	ttc	cac	tac	ttc	ccc	aat	636
Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	
				180					185					190		
ggg	tcc	ctg	gtc	cca	ggg	tcg	gcc	acc	tgt	acg	gtc	atc	aag	ccc	atg	684
Gly	Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	Met	
			195					200					205			
tgg	atc	tac	aat	ttc	atc	atc	cag	gtc	acc	tcc	ttc	cta	ttc	tac	ctc	732
Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	Leu	
		210					215					220				
ctc	ccc	atg	act	gtc	atc	agt	gtc	ctc	tac	tac	ctc	atg	gca	ctc	aga	780
Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	Arg	
	225					230					235					

cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat att	828
Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile	
240 245 250 255	
caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg gtc	876
Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu Val	
260 265 270	
tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc ttc	924
Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu Phe	
275 280 285	
ttc agc ttt gtg gag gag tgg act gaa tcc ctg gct gct gtg ttc aac	972
Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val Phe Asn	
290 295 300	
ctc gtc cat gtg gtg tca ggt gtc tta ttc tac ctg agc tca gct gtc	1020
Leu Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala Val	
305 310 315	
aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca ttc	1068
Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe	
320 325 330 335	
cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat gac	1116
Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp	
340 345 350	
cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc cac	1164
Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His	
355 360 365	
ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cta tgt cag tca	1212
Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys Gln Ser	
370 375 380	
tcc gtg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag atg	1260
Ser Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln Met	
385 390 395	
tca aga aca aac tat caa agc ttc cac ttt aac aaa acc tgaattcttt	1309
Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr	
400 405 410	
cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat aatgtatgcc	1369
ttctcatatg aaattagaga ggtagaatgg ctcttacaac tcatgtaccc attgctagtt	1429
tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac ccaagactgc	1489
ctgattttta gttatctttc cactatccta actgcctcat gcccttcac tagttcatgc	1549
caagaacgtg actggaaagg catggcacct ataccttgat taatttccat taatggaaat	1609

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1658

<210> 8

<211> 412

<212> PRT

<213> Homo sapiens

<400> 8

Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu Glu
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Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala Phe
20 25 30

Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val Val
35 40 45

Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val Cys
50 55 60

Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr Tyr
65 70 75 80

Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly Met
85 90 95

Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe Gly
100 105 110

Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys Phe
115 120 125

Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val Ala
130 135 140

Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg Ala
145 150 155 160

Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser Leu
165 170 175

Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn Gly
180 185 190

Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met Trp
195 200 205

Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu Leu
210 215 220

Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg Leu
225 230 235 240

Lys	Lys	Asp	Lys	Ser 245	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	Ile 255	Gln
Arg	Pro	Cys	Arg 260	Lys	Ser	Val	Asn	Lys	Met	Leu	Phe	Val	Leu 270	Val	Leu
Val	Phe	Ala 275	Ile	Cys	Trp	Ala	Pro 280	Phe	His	Ile	Asp	Arg 285	Leu	Phe	Phe
Ser	Phe 290	Val	Glu	Glu	Trp	Thr 295	Glu	Ser	Leu	Ala	Ala 300	Val	Phe	Asn	Leu
Val 305	His	Val	Val	Ser	Gly 310	Val	Leu	Phe	Tyr	Leu 315	Ser	Ser	Ala	Val	Asn 320
Pro	Ile	Ile	Tyr	Asn 325	Leu	Leu	Ser	Arg	Arg 330	Phe	Gln	Ala	Ala	Phe 335	Gln
Asn	Val	Ile	Ser 340	Ser	Phe	His	Lys	Gln 345	Trp	His	Ser	Gln	His 350	Asp	Pro
Gln	Leu	Pro 355	Pro	Ala	Gln	Arg	Asn 360	Ile	Phe	Leu	Thr	Glu 365	Cys	His	Phe
Val 370	Glu	Leu	Thr	Glu	Asp	Ile 375	Gly	Pro	Gln	Phe	Leu 380	Cys	Gln	Ser	Ser
Val 385	His	Asn	Ser	His	Leu 390	Pro	Thr	Ala	Leu	Ser 395	Ser	Glu	Gln	Met	Ser 400
Arg	Thr	Asn	Tyr	Gln 405	Ser	Phe	His	Phe	Asn 410	Lys	Thr				

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<210> 9
<211> 1594
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (55)..(942)
<223> IGS4A truncated DNA long version
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Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys
          5              10              15

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cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg	153
Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu	
20 25 30	
gcc ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct	201
Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser	
35 40 45	
gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg	249
Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu	
50 55 60 65	
gtg tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac	297
Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn	
70 75 80	
tac tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt	345
Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu	
85 90 95	
gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg	393
Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu	
100 105 110	
ttc ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg	441
Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val	
115 120 125	
tgc ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac	489
Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr	
130 135 140 145	
gtg gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc	537
Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg	
150 155 160	
cgg gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc	585
Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe	
165 170 175	
tcc ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc	633
Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro	
180 185 190	
aat ggg tcc ctg gtc cca ggt tcg gcc acc tgt acg gtc atc aag ccc	681
Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro	
195 200 205	
atg tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac	729
Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr	
210 215 220 225	

ctc ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc 777
Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu
230 235 240

aga cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat 825
Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn
245 250 255

att caa aga ccc tgc aga aaa tca gtc aac aag atg ctg tct ttg tgg 873
Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu Trp
260 265 270

agg agt gga gtg aat ccc tgg ctg ctg tgt tca acc tcg tcc atg tgg 921
Arg Ser Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met Trp
275 280 285

tgt cag gtg tct tct tct acc tgagctcagc tgtcaacccc attatctata 972
Cys Gln Val Ser Ser Ser Thr
290 295

acctactgtc	tgcgcgcttc	caggcagcat	tccagaatgt	gatctcttct	ttccacaaac	1032
agtggcactc	ccagcatgac	ccacagttgc	cacctgccc	gcggaacatc	ttcctgacag	1092
aatgccactt	tgtggagctg	accgaagata	taggtcccca	attcccatgt	cagtcaccca	1152
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aacttcagag	aggaacatcc	cataatgtat	gccttctcat	atgatattag	agaggtagaa	1332
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agagttagat	ctggtttcaa	aaccaagac	tgcttgattt	ttagttatct	ttccactatc	1452
ctaactgcct	catgcccctt	cactagttca	tgccaagaac	gtgactggaa	aggcatggca	1512
cctatacctt	gattaatttc	cattaatgga	aatggttcgt	cctgagtcac	ctacgttccg	1572
agtcaggctg	tcactcctac	ta				1594

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<210> 10
<211> 296
<212> PRT
<213> Homo sapiens
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Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val
 35 40 45
 Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val
 50 55 60
 Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr
 65 70 75 80
 Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu
 85 90 95
 Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe
 100 105 110
 Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr
 115 120 125
 Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg
 130 135 140
 Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg
 145 150 155 160
 Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu
 165 170 175
 Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe
 180 185 190
 Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys
 195 200 205
 Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe
 210 215 220
 Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala
 225 230 235 240
 Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala
 245 250 255
 Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu
 260 265 270
 Trp Arg Ser Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met
 275 280 285
 Trp Cys Gln Val Ser Ser Ser Thr
 290 295

<210> 11
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (64)..(942)
 <223> IGS4A truncated DNA short version

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 ggctcagctt gaaacagagc ctcgtaccag gggaggctca ggccttggat tttaatgtca 60

ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa cta 108
 Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu
 1 5 10 15

gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156
 Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala
 20 25 30

ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg 204
 Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val
 35 40 45

gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg 252
 Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val
 50 55 60

tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac 300
 Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr
 65 70 75

tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt gga 348
 Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly
 80 85 90 95

atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc 396
 Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe
 100 105 110

ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg tgc 444
 Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys
 115 120 125

ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac gtg 492
 Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val
 130 135 140

gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg 540
 Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg
 145 150 155

gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc tcc 588
 Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser
 160 165 170 175

ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc aat 636
 Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn
 180 185 190

ggg tcc ctg gtc cca ggt tgc gcc acc tgt acg gtc atc aag ccc atg 684
 Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met
 195 200 205

tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac ctc 732
 Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu
 210 215 220

ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc aga 780
 Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg
 225 230 235

cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat att 828
 Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile
 240 245 250 255

caa aga ccc tgc aga aaa tca gtc aac aag atg ctg tct ttg tgg agg 876
 Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu Trp Arg
 260 265 270

agt gga gtg aat ccc tgg ctg ctg tgt tca acc tgc tcc atg tgg tgt 924
 Ser Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met Trp Cys
 275 280 285

cag gtg tct tct tct acc tgagctcagc tgtcaacccc attatctata 972
 Gln Val Ser Ser Ser Thr
 290

acctactgtc tcgccgcttc caggcagcat tccagaatgt gatctcttct ttccacaaac 1032
 agtggcactc ccagcatgac ccacagttgc cacctgcccc gcggaacatc ttcctgacag 1092
 aatgccactt tgtggagctg accgaagata taggtcccc attcccatgt cagtcatcca 1152
 tgcacaactc tcacctcccc acagccctct ctagtgaaca gatgtcaaga acaaactatc 1212
 aaagcttcca ctttaacaaa acctgaattc tttcagagct gactctcctc tatgcctcaa 1272
 aacttcagag aggaacatcc cataatgtat gccttctcat atgatattag agaggtagaa 1332
 tggctcttac aactcatgta ccatttgcta gttttttttt ttttaataaac gtgaaaactg 1392
 agagttagat ctggtttcaa aaccaagac tgcctgattt ttagttatct ttccactatc 1452
 ctaactgcct catgcccctt cactagttca tgccaagaac gtgactggaa aggcatggca 1512

cctatacctt gattaatttc cattaatgga aatgggttcgt cctgagtcac ctacgttccg 1572

agtcaggctg tcactcctac ta

1594

<210> 12

<211> 293

<212> PRT

<213> Homo sapiens

<400> 12

Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu Glu
1 5 10 15

Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala Phe
20 25 30

Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val Val
35 40 45

Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val Cys
50 55 60

Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr Tyr
65 70 75 80

Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly Met
85 90 95

Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe Gly
100 105 110

Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys Phe
115 120 125

Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val Ala
130 135 140

Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg Ala
145 150 155 160

Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser Leu
165 170 175

Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn Gly
180 185 190

Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met Trp
195 200 205

Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu Leu
210 215 220

Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg Leu
 225 230 235 240

Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile Gln
 245 250 255

Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu Trp Arg Ser
 260 265 270

Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met Trp Cys Gln
 275 280 285

Val Ser Ser Ser Thr
 290

<210> 13
 <211> 26
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Degenerated
 primer

<220>
 <221> modified_base
 <222> (21)
 <223> a, c, g or t

<220>
 <221> modified_base
 <222> (24)
 <223> a, c, g or t

<400> 13
 ctcacatcttcg cggtgggcrc ngyngg

<210> 14
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Degenerated
 primer

<220>
 <221> modified_base
 <222> (22)
 <223> c or Inosine

<220>
 <221> modified_base
 <222> (25)
 <223> a, c, g or t

<220>
 <221> modified_base
 <222> (28)
 <223> a, c, g or t

<400> 14
 ggccaggcag cgctccgcgc tnarncyngc d

31

<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Degenerated
 primer

<400> 15
 gaartartag ccrccgrcagc cw

22

<210> 16
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 16
 ccatacctaatac gactcact atagggc

27

<210> 17
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 17
 actcactata gggctcgagc ggc

23

<210> 18
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 18
 ggatcccaaa taagaaaggg tagttgc

27

<210> 19
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 19
 aaagggtagt tgcgccacat ctcataagac

29

<210> 20
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 20
 aggtctatga gatgtggcgc aactaccct

29

<210> 21
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 21
 atgtggcgca actacccttt cttatttggg

30

<210> 22
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Degenerated
 primer

<400> 22
 cggaagttgg cggacacgrv rttrta

26

<210> 23
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 23
 gctcagcttg aaacagagcc tcgtacc

27

<210> 24
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 24
 ccatgtggat ctacaatttc atcatcc

27

<210> 25
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 25
 aagacaaatc tcttgaggca gatgaaggg

29

<210> 26
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 26
 gatgctgttt gtcttggtct tagtgtttgc 30

<210> 27
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 27
 ggatgatgaa attgtagatc cacatgggc 29

<210> 28
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 28
 tgtggagaag tctctcaaag tgtgg 25

<210> 29
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 29
 tagtaggagt gacagcctga ctcggaacg 29

<210> 30
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 30
 aacgtagatg actcaggacg aaccatttcc

30

<210> 31
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 31
 tcgtaccagg ggaggctcag gc

22

<210> 32
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 32
 cctcttcagc ctggcggtct ctg

23

<210> 33
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 33
 ggaggcgaag cacacggtct ca

22

<210> 34
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> misc_binding
 <222> (1)
 <223> Labeled with 6-carboxyfluorescein

<220>
 <221> misc_binding
 <222> (34)
 <223> Labeled with
 N,N,N',N'-tetramethyl-6-carboxyrhodamin

<400> 34
 agatgtggcg caactaccct ttcttggtcg ggcc

34

<210> 35
 <211> 7
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Illustrative
 mammalian C-terminal sequence

<220>
 <223> C-term amidated

<400> 35
 Phe Leu Phe Arg Pro Arg Asn
 1 5